THERAPEUTICALLY USEFUL MOLECULES

The present invention relates to therapeutically useful molecules, in particular to T cell receptors (TCRs) which may be introduced into a patient's own T cells in order to direct the T cells to kill cancer cells within the patient, particularly cancer cells which express the Wilms Tumour antigen-1 (WT1).

The listing or discussion of a prior-published document in this specification should not necessarily be taken as an acknowledgement that the document is part of the state of the art or is common general knowledge. All of the documents referred to in this specification are hereby incorporated by reference.

There is evidence that anti-tumour cytotoxic T lymphocytes (CTL) play an important role *in vivo*. Tumour reactive CTL have been shown to mediate tumour regression in animal models (Kast *et al* (1989) *Cell* **59**, 603-614) and in man (Kawakami *et al* (1994) *Proc. Natl. Acad. Sci. USA* **91**, 6458-6462; Dudley (2002) *Science* **298**, 850-854). As with all types of anti-tumour therapy, a problem that needs to be overcome is that the therapy must destroy or inactivate the target tumour cells to a useful extent but that the therapy must not destroy or inactivate non-tumour cells to a deleterious extent. In other words, it is desirable if the therapy is selective for tumour cells to a beneficial extent.

Much of the current work on immunotherapy of cancer makes use of the fact that certain tumours express polypeptides which are not expressed in the equivalent non-tumour tissue, or makes use of the fact that the tumour expresses a mutant form of a polypeptide which is not expressed in the non-tumour tissue. However, it is not always possible to identify polypeptides in a tumour which fall into this category, and so other target polypeptides which can form the basis of an immunotherapeutic approach have been identified.

In adults, expression of WT1, an embryonic transcription factor, has been observed in renal podocytes, in the testis, in the ovary, in breast myoepithelial

cells and in some $CD34^+$ stem cells in the bone marrow. Aberrant expression was observed in breast cancer, ovarian cancer, melanoma, lung cancer, colon cancer, thyroid cancer, head and neck cancer, glioblastoma, sarcoma and leukaemia including CML and AML (see, for example, Menssen *et al* (1995) *Leukaemia* **9**, 1060-1067; Inoue *et al* (1997) *Blood* **89**, 1405-1412; Inoue *et al* (1996) *Blood* **88**, 2267-2278; Inoue *et al* (1998) *Blood* **91**, 2969-2976; Menssen *et al* (1997) *Int. J. Cancer* **70**, 518-523; Menssen *et al* (1995) *Leukemia* **9**, 1060-1067; Ogawa *et al* (1998) *Transplant* **21**, 527-527; Rodeck *et al* (1994) *Int. J. Cancer* **59**, 78-82; Silberstein *et al* (1997) *Proc. Natl. Acad. Sci. USA* **94**, 8132-8137; Tamaki *et al* (1996) *Blood* **88**, 4396-4398; Viel *et al* (1994) *Int. J. Cancer* **57**, 515-521; Menssen (2000) *J. Cancer Res. Clin. Oncol.* **126**, 226-232; Miyoshi (2002) *Clin. Cancer Res.* **8**, 1167-1171; Oji (1999) *Jpn J. Cancer Res.* **90**, 194-204; Oji (2003) *Cancer Sci.* **94**, 523-529; Oji *et al* (2003) *Cancer Sci.* **94**, 606-611; Oji *et al* (2003) *Cancer Sci.* **94**, 712-717; and Ueda (2003) *Cancer Sci.* **94**, 271-276.

As described in our patent application WO00/26249, using an unconventional approach employing allo-MHC-restricted CTL, we identified peptide epitopes in the WT1 polypeptide which may be presented by HLA-A2 class I molecules and displayed on the surface of tumour cells expressing these proteins endogenously. HLA-A2 negative responder individuals were used as a source of CTL specific for peptides presented by HLA-A2 class I molecule, and this approach allows identification of HLA-A2 presented peptides independent of possible tolerance of autologous CTL.

One of the peptide epitopes disclosed in WO00/26249 is RMFPNAPYL (which we have also termed pWT126), and we have previously described a CTL which is able to: kill HLA-A2-positive targets coated with the WT1-derived peptide pWT126 (Gao *et al* (2000) *Blood* **95**, 2198-2203); kill fresh HLA-A2-positive leukaemia cells expressing WT1 (Gao *et al* (2000) *Blood* **95**, 2198-2203); kill HLA-A2-positive leukemia CFU progenitor cells (Gao *et al* (2000) *Blood* **95**, 2198-2203; Bellantuono *et al* (2002) *Blood* **100**, 3835-3837); kill HLA-A2-positive leukaemia LTC-IC stem cells (Bellantuono *et al* (2002) *Blood* **100**, 3835-

3837); kill HLA-A2-positive NOD/SCID leukaemia initiating cells (Gao *et al* (2003) *Transplantation* 75, 1429-1436); and do not kill normal HLA-A2-positive NOD/SCID engrafting hematopoietic stem cells (Gao *et al* (2003) *Transplantation* 75, 1429-1436). However, none of these publications give molecular information concerning the TCR present in the CTL, and the particular CTL line mentioned in the publications has not been made available to the public in any way and so the structure of the TCR is unknown and could not be derived by the skilled person (since the CTL line was not publicly available).

The present inventors have now cloned a TCR that is specific to RMFPNAPYL, a peptide of WT1 which is presented by HLA-A2 class I molecules, and have shown that introducing the TCR into either CD4-positive or CD8-positive T cells confers on the engineered T cells the ability to kill cancer cells which express WT1 endogenously. In addition, the inventors have defined the molecular structure of the TCR, identified the complementarity determining regions (CDRs), and describe how to make recombinant TCRs which are believed to retain the same specificity of the parent molecule.

The TCRs may usefully be introduced into a T cell derived from a patient (preferably an HLA-A2-positive patient) suffering from a malignancy (where the patient's tumour cells express WT1), and the engineered T cell introduced into the patient in order to combat the malignancy. In particular, it is proposed to take T cells from patients with breast cancer, colon cancer, lung cancer, other solid cancers or leukaemia, transduce them *in vitro* with a retroviral vector containing the TCR genes, and re-infuse the transduced T cells into the patients. The credibility of this approach is confirmed by the demonstration in the Examples that the WT1-specific TCR genes can be transferred into human T cells, that the genes give raise to TCR expression on the surface of recipient T cells, that the recipient T cells can kill HLA-A2-positive target cells coated with the pWT126 peptide and HLA-A2-positive tumour cells expressing WT1 endogenously.

The general structure of T cell receptors (TCRs), their domain structure and the organisation of genes that encode them is well known, for example see Chapter 11 in Immunology, second edition (1994), by Janis Kuby, W H Freeman & Co, New York, USA, and Garcia *et al* (1999) *Ann. Rev. Immunol.* **17**, 369-397. One common class of natural TCRs is the αβ class in which the TCRs are made up of a separate alpha chain and a separate beta chain which form a heterodimer which is T cell membrane associated. Each alpha and beta chain is made up of regions which, in order from the N terminus to the C terminus are a leader sequence, a variable region, a constant region, a connecting sequence, a transmembrane region and a cytoplasmic tail region (see Figure 14 for a graphical representation of αβ TCR structure). The variable region of the alpha chain is called the Vα region and the variable region of the beta chain is called the Vβ region. Similarly, the constant region of the alpha chain is called the Cα region and the constant region of the beta chain is called the Cβ region. The job of the αβ TCR is to recognise and bind to a peptide presented in a HLA molecule of a cell in the body. Generally speaking, the TCR cannot recognise and bind the peptide unless it is presented by a particular HLA molecule, and the TCR cannot recognise a HLA molecule unless it is presenting the specific peptide. T cells harboring a specific TCR will target cells which are presenting a specific peptide in a particular HLA molecule on a cell (ie a peptide-HLA complex), and this is the main principle of T cell-based immunity.

The peptide-HLA complex is recognised by the combined V regions of the alpha and beta chains of the TCR. In particular, it is the complementarity determining regions (CDRs) of the V regions which mediate recognition of the peptide-HLA complex. The V region of the alpha and beta chains of the natural TCR are made up of, in order in an N-terminal to C-terminal direction, FR1, CDR1, FR2, CDR2, FR3 and CDR3, where FR stands for "framework region" and CDR stands for "complementarity determining region". The FRs and CDRs of the alpha and beta chains are different.

From the predicted amino acid sequences of the alpha and beta chains of the TCR cloned as mentioned above, the inventors have determined the FRs and CDRs of the alpha and beta chains (see Figures 2 and 4). With the knowledge of the CDR sequences, it is possible to produce chimaeric TCRs in which the CDRs are grafted onto framework regions with which the CDRs are not naturally associated, and it is also possible to produce single chain TCR molecules, and in both cases the molecules retain substantially the same binding affinity for the peptide-HLA complex as the parent molecule, as is described in more detail below.

A first aspect of the invention provides a T cell receptor (TCR) molecule containing an alpha chain portion and a beta chain portion wherein the alpha chain portion contains three complementarity determining regions (CDRs):

CDR1α: SSYSPS

CDR2α: YTSAATL

CDR3α: VVSPFSGGGADGLT or comprising or consisting of SPFSGGGADGLT

and the beta chain portion contains three complementarity determining regions (CDRs):

CDR1β: DFQATT

CDR2β: SNEGSKA

CDR3β: comprising SARDGGEG, or comprising or consisting of RDGGEGSETQY or wherein up to three amino acid residues in one or more of the CDRs are replaced by another amino acid residue.

It should be noted that in some nomenclature systems the CDR3 of the β chains may be defined to be longer than in the nomenclature system used in the Immunogenetics (IMGT) database described below. Also, in some nomenclature systems the CDR3 of the α chains may be defined to be shorter than in the IMGT system. Similarly, the constant portion may or may not include framework residues flanking the CDR3 region in the different nomenclature systems.

Thus, in one embodiment using the IMGT system CDR3α may have the amino

acid sequence VVSPFSGGGADGLT and the constant portion includes the framework amino acid sequence FGKGTHLIIQP (see Figure 5).

In another embodiment, using the Garcia nomenclature system (Garcia *et al* (1999) *Ann. Rev. Immunol.* **17**, 369-397, incorporated herein by reference) CDR3α comprises or consists of the amino acid sequence SPFSGGGADGLT, the framework region immediately C-terminal to this has the amino acid sequence FGKGTHLIIQP and the constant region begins with the amino acid sequence YIQNP ... (see Figure 5).

In one embodiment using the IMGT nomenclature system, CDR3β may have the amino acid sequence SARDGGEG and the constant region immediately C-terminal to this includes the framework amino acid sequence SETQY ... (Figure 4).

In another embodiment, using the Garcia nomenclature system as above, CDR3β comprises or consists of the amino acid sequence RDGGEGSETQY and the framework region immediately C-terminal to this has the amino acid sequence FGPGTRLLVL and the immediately C-terminal constant region begins with the amino acid sequence EDLKN ... (see Figure 6).

It will be appreciated that the skilled person can readily design and synthesise TCRs according to the invention using either or any nomenclature systems provided that the framework region (ie region not replaced by the CDRs) is compatible with the CDRs as is well known in the act.

The standard IUPAC one letter amino acid code is used throughout the specification. For the avoidance of doubt, a reference to a "particular" or "given" CDR means any CDR with the amino acid sequence given above or wherein up to three amino acids have been replaced by another amino acid residue.

By "TCR molecule" we include any molecule which contains the given CDRs and

also contains FRs suitably situated within the molecule so that the CDRs form a recognition site (combining site) which is able to bind to HLA-A2 presenting the peptide RMFPNAPYL (ie a HLA-A2/RMFPNAPYL complex).

It is particularly preferred if the TCR molecules contain the precise CDR amino acid sequences as given above and in Figures 2 and 4 and in Figures 5 and 6. Where a variant to this precise sequence is present, it preferably varies by one or two or three (preferably one or two) amino acids in one or two or three or four or five or all six CDRs. Typically, in these variants, the amino acids which are replaced are replaced with conservative amino acids. By conservative amino acids we include the groupings: G, A; S, A, T; F, Y, W; D, E; N, Q; and I, L, V.

A method for making and selecting TCR molecules which have CDRs which vary from the precise CDR sequences given in Figures 2 and 4 and in Figures 5 and 6 is given below.

The amino acid sequences, including V regions (and therefore FRs), of numerous TCR alpha chains and TCR beta chains are well known in the art, some of which are described in the IMGT (Immunogenetics) database at http://imgt.cines.fr. See also Lefranc (2003) *Dev. Comp. Immunol.* **27**, 55-77. The structural basis of T cell recognition is reviewed in Garcia *et al* (1999) *Ann. Rev. Immunol.* **17**, 369-397, and the information contained therein may be used to design and synthesise CDR-grafted TCRs (and CDRs defined on the basis of this nomenclature are noted above). Preferably, the FRs into which the particular CDRs are grafted are FRs of human TCR alpha or beta chains. Conveniently, the alpha chain CDRs are grafted into alpha chain FRs, and beta chain CDRs are grafted to beta chain FRs. Typically, the three CDRs in the alpha chain and the three CDRs in the beta chain replace, in order, CDRs in other human alpha and beta chains, respectively. See Lefranc (2003) *Dev. Comp. Immunol.* **27**, 55-77.

Typically, T cells expressing the TCR molecule recognise the HLA-A2 presenting peptide RMFPNAPYL with substantially the same avidity as the TCR molecule

which consists of the alpha and beta chains as described in Figures 2 and 4. This can be measured by retroviral-mediated transfer of the TCR into T cells followed by peptide titration experiments with the TCR-transduced T cells as outlined, for example, in Gao *et al* (2000) *Blood* **95**, 2198-2203.

The TCR molecule preferably contains an alpha chain portion containing, in N-terminal to C-terminal order, FR1α-CDR1α-FR2α-CDR2α-FR3α-CDR3α, and a beta chain portion containing, in N-terminal to C-terminal order, FR1β-CDR1β-FR2β-CDR2β-FR3β-CDR3β as shown in Figures 2 and 4, respectively and in Figures 5 and 6, respectively. Typically, the TCR molecule contains the V region of both the alpha chain and the beta chain of the TCR polypeptide chains shown in Figures 2 and 4, and in Figures 5 and 6.

In a preferred embodiment, the alpha chain portion and the beta chain portion are present on different polypeptide chains. Typically, the TCR molecule contains an alpha chain which contains the V region and the C region of the polypeptide chain shown in Figure 2 (or Figure 5), and also contains a beta chain which contains the V region and C region of the polypeptide chain shown in Figure 4 (or Figure 6). Preferably, the TCR molecule consists of a molecule containing the complete alpha chain shown in Figure 2 and the complete beta chain shown in Figure 4. Typically, however, the leader sequence is cleaved off the mature alpha chain and beta chain.

In a further embodiment, the alpha chain portion and the beta chain portion of the TCR molecule are present in the same polypeptide chain. Single chain TCR molecules are described in Chung *et al* (1994) *Proc. Natl. Acad. Sci. USA* **91**, 12654-12658, and the principles described therein may readily be applied to the production of single chain TCR molecules which contain the specified CDRs. Typically, the single chain TCR molecules contain the Vα, Vβ and Cβ domains fused in the same polypeptide chain, and typically in that order (from N-terminus to C-terminus). For expression of a single chain TCR it is useful to provide a construct encoding the constant domain of the TCR alpha chain.

An additional strategy is described in Boulter *et al* (2003) *Protein Eng.* **16**, 707-711 in which a new disulphide bond is introduced between a threonine in the constant region of the alpha chain and a serine in the constant region of the beta chain (by replacing these residues with a cysteine. The disulphide bond in the TCR connecting peptide may be removed or may remain in place.

The two-chain TCR molecules of the invention (eg ones which contain the alpha and beta chains whose amino acid sequence is given in Figures 2 and 4) or chimaeric TCRs which contain the specific CDRs as described above may be used to introduce to create antigen-specific CTL as described in more detail below (by using polynucleotides that encode the relevant chains). Similarly, the single chain TCRs may also be used for this purpose, and have the advantage that they do not pair with endogenous TCRs. Single chain TCRs may also be used as soluble constructs in a way similar to antibodies. In this case, the single chain constructs do not contain a transmembrane region (see Chung *et al supra* and Boulter *et al supra*).

A second aspect of the invention provides a polynucleotide encoding the alpha chain portion as defined in the first aspect of the invention. A third aspect of the invention provides a polynucleotide encoding the beta chain portion as defined in the first aspect of the invention. As discussed above, in a particularly preferred embodiment of the invention, the alpha chain portion and the beta chain portion are present on different polypeptide chains, and it is convenient (but not mandatory) that each polypeptide is encoded by a separate polynucleotide. Preferred polynucleotides encoding the alpha and beta chains are described in Figures 1 and 2, respectively. Alternatively, the two polypeptides may be encoded on the same polynucleotide, in which case the two coding regions may be linked by an (Internal Ribosome Entry Site) IRES sequence, and typically would have its own translational start and stop codons. Typically, such constructs contain two promoters, one for each TCR chain.

As discussed above, in an alternative embodiment the alpha chain portion and the beta chain portion are present in the same polypeptide, in which case a single polynucleotide may encode the single chain polypeptide.

In any event, the polynucleotide may be DNA or RNA, and it may or may not contain introns. Typically, the polynucleotide does not contain introns within the region that codes for the polypeptide of interest. It will be appreciated that different polynucleotides may encode the same polypeptide because of the degeneracy of the genetic code.

The invention also provides an expression vector that contains the polynucleotide of the invention. Such expression vectors, when present in a suitable host cell, allow for the expression of the polypeptide(s) of interest. Preferably, the expression vector is an expression vector capable of expressing a polypeptide in a mammalian cell. More preferably, the expression vector is one which is able to express a polypeptide in a T cell, such as a human CTL. Typically, the expression vectors contain a promoter which is active in particular cell types, and which may be controllable (eg inducible).

The vector is suitably a retroviral vector which is capable of transfection into a mammalian host cell such as a human T cell. Typically, the vector is a lentiviral vector.

A further aspect of the invention provides a host cell comprising a polynucleotide of the invention or a vector of the invention. The host cell may contain a polynucleotide or vector which encodes only the alpha chain portion or only the beta chain portion. However, if the host cell is to produce a TCR molecule of the invention, it contains one or more polynucleotides or vectors which encode both the alpha chain portion and the beta chain portion.

The host cell may be any cell such as a bacterial cell, yeast cell, insect cell, plant cell or mammalian cell, and methods of introducing polynucleotides into such

cells are well known in the art. Typically, bacterial cells, such as *Escherichia coli* cells are used for general propagation and manipulation of the polynucleotides and vectors of the invention. Other host cells may be used to express the TCR molecules of the invention and, in particular, the cell may be a mammalian cell such as a human cell. As described below in relation to the therapeutic methods using the TCR molecules of the invention, it is particularly desirable if the host cell is a T cell such as (and preferably) a T cell derived from a patient to be treated, typically a patient with a WT1-expressing malignancy.

Typically, a retroviral vector (or, as the case may be vectors) encoding the TCR molecule of the invention is used based on its ability to infect mature human $CD4^+$ or $CD8^+$ T lymphocytes and to mediate gene expression: the retroviral vector system Kat is one preferred possibility (see Finer *et al* (1994) *Blood* **83**, 43). High titre amphotrophic retrovirus are used to infect purified $CD8^+$ T lymphocytes isolated from the peripheral blood of tumour patients following a protocol published by Roberts *et al* (1994) *Blood* **84**, 2878-2889, incorporated herein by reference. Anti-CD3 antibodies are used to trigger proliferation T cells, which facilitates retroviral integration and stable expression of single chain TCRs. A combination of anti-CD3 and anti-CD8 antibodies may be more effective than anti-CD3 antibodies alone. Other suitable systems for introducing genes into CTL are described in Moritz *et al* (1994) *Proc. Natl. Acad. Sci. USA* **91**, 4318-4322, incorporated herein by reference. Eshhar *et al* (1993) *Proc. Natl. Acad. Sci. USA* **90**, 720-724 and Hwu *et al* (1993) *J. Exp. Med.* **178**, 361-366 also describe the transfection of CTL. The commercially available Nuclofactor system, provided by AMAXA, Germany may be used to transfect T cells. Retroviral transduction of human $CD8^+$ T cells is described in Stanislawski (2001) *Nat. Immunol.* **2**, 962.

Methods of cloning and genetic manipulation are well known in the art and are described in detail in standard manuals such as Sambrook & Russell (2001) Molecular Cloning, a laboratory manual, Cold Spring Harbor Press, Cold Spring Harbor, NY, USA.

Patients suffering from a WT1-expressing malignancy may be treated by the introduction of the TCR molecule of the invention into their own T cells (or T cells from a donor), followed by the introduction of these engineered cells into the patient. Thus, a further aspect of the invention provides a method of combating a WT-1 expressing malignancy in a patient, the method comprising introducing into the patient a T cell, preferably derived from the patient, which is modified to express the TCR molecule of the invention. Typically, (1) T cells are obtained from the patient, (2) a polynucleotide or polynucleotides encoding and capable of expressing the TCR molecule of the invention are introduced into the T cells *ex vivo* and (3) the engineered T cells are introduced into the patient. It is particularly preferred if the T cells are the patient's T cells (ie autologous).

It is particularly preferred if the patient is HLA-A2 positive.

In other words, the specificity of the T cell, preferably autologous T cell, is changed by the introduction of the TCR molecule of the invention.

The T cells (for example of the patient) are typically isolated from peripheral blood mononuclear cells (PBMCs), and may be $CD4^+$ and $CD8^+$ cells. Typically, the cells are activated using an antibody (eg an anti-CD3 or anti-CD28 antibody) so that they become receptive to transfection, for example with one or more retroviral vectors encoding the TCR molecules of the invention. The number of cells isolated, transfected and returned to the patient may be determined by the physician.

Cells may be taken from a patient after a clinical response, cryopreserved, transfected and re-infused if the same patient relapses.

Whether or not a malignancy is one which expresses WT1 may be determined, for example using reverse transcriptase-polymerase chain reaction (RT-PCR) or using intracellular staining techniques for the WT1 protein (which may be anti-WT1 antibodies).

The patient is preferably a human patient although animals may be used in a research situation. It is particularly preferred that the patient is HLA-A2 positive. Whether or not a patient is HLA-A2 positive can be determined by methods well known in the art.

Typically, the patient is suffering from any one or more of leukaemia, breast cancer, colon cancer, lung cancer, ovarian cancer, melanoma, thyroid cancer, head and neck cancer, glioblastoma, and sarcoma.

A further aspect of the invention provides the use of a T cell, preferably a patient derived T cell, which is modified to express the TCR molecule of the invention in the manufacture of a medicament for combating a WT1-expressing malignancy in the patient.

As discussed above, TCR molecules in which one or more of the CDRs differ in sequence from the precise CDR sequences given in Figures 2 and 4 form part of the invention. Preferably, such TCR molecules are able to recognise the HLA-A2/RMFPNAPYL complex more effectively than a TCR molecule with the precise CDR sequences. Thus, a further aspect of the invention provides a method of selecting a TCR molecule with improved binding to an HLA-A2/RMFPNAPYL complex comprising (a) providing a TCR molecule containing an alpha chain portion and a beta chain portion wherein the alpha chain portion contains three complementarity determining regions (CDRs):

CDR1α: SSYSPS

CDR2α: YTSAATL

CDR3α: VVSPFSGGGADGLT or comprising or consisting of SPFSGGGADGLT

and the beta chain portion contains three complementarity determining regions (CDRs):

CDR1β: DFQATT

CDR2β: SNEGSKA

CDR3β: comprising SARDGGEG or comprising or consisting of RDGGEGSETQY

wherein at least one amino acid residue in one or more of the CDRs as given is replaced with another amino acid residue, (b) determining whether the TCR molecule binds to an HLA-A2/RFMPNAPYL complex with greater affinity than a TCR molecule without the replacement amino acid(s), and (c) selecting a molecule which binds with greater affinity. Preferably, the CDR3β has the amino acid sequence given above in relation to the first aspect of the invention.

TCR molecules with altered CDRs can readily be made by protein engineering methods. For example, a TCR display library may be made in which the alpha chain and/or beta chain CDR regions are mutagenised and the TCR molecules displayed using retroviral transduction on the surface of a T cell lymphoma (see Kessels *et al* (2000) *Proc. Natl. Acad. Sci. USA* **97**, 14578-14583), or on the surface of a yeast or a bacteriophage. A HLA-A2/RMFPNAPYL complex may be used to select cells or bacteriophages which bind the complex with high affinity by virtue of the TCR molecule that they present. TCR molecules which have a higher binding affinity (lower K_D) than a TCR molecule with the precise CDR sequences are selected for further study.

The invention will now be descried in more detail by reference to the following figures and non-limiting examples.

Figure 1 shows the nucleotide coding sequence of the pWT126-specific TCR-alpha chain (Vα-1.5).

Figure 2 shows the protein sequence of the pWT126-specific TCR-alpha chain (Vα-1.5). The position of the CDRs, FRs and constant region are marked. The leader sequence is shown in bold.

Figure 3 shows the nucleotide coding sequence of the pWT126-specific TCR-beta chain (Vβ-2.1)..

Figure 4 shows the protein sequence of the pWT126-specific TCR-beta chain (Vβ-2.1). The position of the CDRs, FRs and constant region are marked.

Figure 5 shows the same protein sequence as in Figure 2 but the start position of the constant region is indicated to be in a different place. The CDR sequence in this figure, starting after C, is based on IMGT nomenclature (primary sequence based). The Garcia nomenclature is based on structure and does not include the VV after the C (ie it starts SPF...). Va8.2 means variable alpha 8.2 gene segment and J45 means joining 45 gene segment.

Figure 6 shows the same protein sequence as in Figure 4 except that CDR3β is indicated as being longer and the start position of the constant region is indicated to be in a different place. The CDR sequence in this figure, starting after C, is based on IMGT nomenclature (primary sequence based). The Garcia nomenclature is based on structure and does not include the SA after the C (ie it starts RDGG...). J2.5 refers to joining 2.5 gene segment.

Figure 7 is a diagram showing retroviral vectors containing TCR genes. The TCR alpha and beta chains were inserted into the retroviral vector pMP71 (Engels *et al* (2003) *Human Gene Ther.* **14**, 1155-1168 for gene transfer into human T cells. LTR is a long terminated repeat. PRE is posttranscriptional regulatory element.

Figure 8 is a diagram showing retroviral TCR gene transfer into human T cells. Peripheral blood lymphocytes were activated with anti-CD3 antibodies, IL-2 and IL-7, followed 3 days later by transduction with retroviral vectors encoding the WT1-specific TCR. TCR expression was monitored at day 6 using antibodies specific for the TCR-V-beta 2.1 (present in the transferred TCR). Mock transduced T cells show the percentage of un-manipulated human T cells expressing V-beta 2.1. After transduction both CD8-positive and CD8-negative

(i.e. CD4-pos) T cells have an increased percentage of V-beta 2.1 cells. V-beta 2.1 DNA and amino acid sequences are shown in Figures 3 and 4.

Figure 9 shows that repeated stimulation of TCR-transduced T cells (as shown in Fig. 8) with T2 cells presenting the pWT126 peptide leads to an expansion of CD8-positive T cells expressing V-beta 2.1.

Figure 10 shows that TCR-transduced T cells (as shown in Figs. 8 and 9) stain with HLA-A2/pWT126 tetramers.

Figure 11 shows that TCR-transduced T cells (as shown in Fig. 8 and 9) kill the HLA-A2-positive T2 cells coated with the pWT126 peptide, but not T2 cells coated with the A2-binding pWT235 control peptide. The T cells also kill the HLA-A2-positive BV173 leukaemia cells expressing WT1 endogenously.

Figure 12 shows that purified TCR-transduced CD8-positive T cells kill the HLA-A2-positive T2 cells coated with the pWT126 peptide, but not T2 cells coated with the A2-binding pWT235 control peptide. The CD8-positive T cells also kill the HLA-A2-positive BV173 leukaemia cells expressing WT1 endogenously.

Figure 13 shows that a small percentage of purified CD4-positive TCR-transduced T cells stain with HLA-A2/pWT126 tetramers.

Figure 14 shows that purified TCR-transduced CD4-positive T cells kill the HLA-A2-positive T2 cells coated with the pWT126 peptide, but not T2 cells coated with the A2-binding pWT235 control peptide. The CD4-positive T cells also kill the HLA-A2-positive BV173 leukaemia cells expressing WT1 endogenously.

Figure 15 shows that purified TCR-transduced CD8-positive T cells produce IFN-γ after stimulation with the HLA-A2-positive T2 cells coated with the pWT126 peptide, but not T2 cells coated with the A2-binding pWT235 control peptide. Also, the CD8-positive T cells produce IFN-γ after stimulation with the HLA-A2-

positive BV173 leukaemia cells expressing WT1 endogenously.

Figure 16 is a schematic diagram showing the general structure of αβ TCR molecules. The amino acid numbers mentioned do not necessarily correspond to those in Figures 2 and 4.

Schedule of SEQ ID Nos.

1. RMFPNAPYL
2. SSYSPS
3. YTSAATL
4. VVSPFSGGGADGLT
5. SPFSGGGADGLT
6. DFQATT
7. SNEGSKA
8. SARDGGEG
9. RDGGEGSETQY
10. FGKGTHLIIQP
11. YIQNP
12. SETQY
13. FGPGTRLLVL
14. EDLKN
15. Figure 1 nucleotide sequence
16. Figure 2 (and Figure 5) amino acid sequence
17. Figure 3 nucleotide sequence
18. Figure 4 (and Figure 6) amino acid sequence

Example 1: Functionally active T cell receptor (TCR) specific for the WT-1-derived peptide pWT126 (RMFPNAPYL)

We have cloned a T cell receptor (TCR) that is specific for a peptide (pWT126; RMFPNAPYL) of the Wilms Tumour antigen-1 (WT1) presented by HLA-A2 class I molecules. The WT1 transcription factor is expressed in various human malignancies, including leukaemia, breast cancer, colon cancer, lung cancer, ovarian cancer and others. The CTL from which the TCR was cloned show killing activity against human cancer cells that express WT1, but not against normal human cells that express physiological levels of WT1.

The therapeutic goal is to equip patient T cells with this potent and specific killing activity by transfer of the genes encoding the TCR. For this, we have inserted the TCR genes into retroviral vectors and demonstrated that gene transduced human T cells show killing activity against WT1 expressing human cancer and leukemia cell lines. The specificity profile of this CTL line has been described in several research papers and can be summarized as: (1) Killing of HLA-A2-positive targets coated with the WT1-derived peptide pWT126 (Gao *et al* (2000) *Blood* **95**, 2198-2203); (2) Killing of fresh HLA-A2-positive leukaemia cells expressing WT1 (Gao *et al* (2000) *Blood* **95**, 2198-2203); (3) Killing of HLA-A2-positive leukemia CFU progenitor cells (Gao *et al* (2000) *Blood* **95**, 2198-2203; Bellantuono *et al* (2002) **100**, 3835-3837); (4) Killing of HLA-A2-positive leukaemia LTC-IC stem cells (Bellantuono *et al* (2002) *Blood* **100**, 3835-3837); (5) Killing of HLA-A2-positive NOD/SCID leukaemia initiating cells (Gao *et al* (2003) *Transplantation* **75**, 1429-1436); and (6) No killing of normal HLA-A2-positive NOD/SCID engrafting hematopoietic stem cells (Gao *et al* (2003) *Transplantation* **75**, 1429-1436). We have now shown that human T cells transduced with the WT1-specific TCR display similar specificity as the CTL line from which the TCR was cloned.

The data described in detail in the legends to Figures 1 to 15 indicate that TCR gene transfer into human T cells is feasible and that it leads to the surface expression of the introduced TCR chains. The recipient T cells show killing

activity against HLA-A2-positive targets coated with the pWT126 peptide. The TCR-transduced T cells also kill human tumour cells expressing WT1 endogenously. In addition, the transduced T cells produce IFN-g in an HLA-A2-restricted, peptide-specific fashion. Finally, the transferred TCR can function in CD4-positive helper T cells. These CD4-positive T cells show HLA-A2-restricted, antigen-specific killing activity and antigen-specific cytokine production (not shown). This indicates that TCR gene transfer can be used to confer HLA class I-restricted antigen-specific effector function to both CD8-positive and CD4-positive human T cells.

Example 2: Selection and treatment of a patient

Peripheral blood monocyte cells (PBMCs) are taken from an HLA-A2-positive patient who has a WT1-expressing malignancy. The PBMCs are activated with anti-CD3/CD28 antibodies added to the culture or on beads for 3 days and then transduced with TCR encoding retroviral particles as described in Example 1. At day 5 we can demonstrate that transduced CD4 and CD8 T cells express the introduced TCR. At day 6 we can demonstrate antigen-specific activity of the transduced T cells. At day 6 the transduced T cells are reinfused into the patient.